

# SEQUENCE LISTING

<110> Kazuko, SHINOZAKI  
Mie, KASUGA

<120> Environmental Stress-Tolerant Plants

<130> 382.1029DIV2

<150> JP292348/1998  
US 09/301,217

<151> 1998-10-14  
1999-04-28

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<170> PatentIn Ver. 2.0

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Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
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 Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val Ala Glu Arg  
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 Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu Val Ser Thr  
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Tyr																	
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Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly
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Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp
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Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val
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Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp
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tcg gct tgg cgg cta cga atc ccg gaa tca acc tgt gcc aag gaa atc 506
Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile
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Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys
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Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met
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cgactctaata cctggagtta tcattcacga tagattctta gattgcgact ataaagaaga 180
ag atg gct gta tat gaa caa acc gga acc gag cag ccg aag aaa agg 227
Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg
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aaa tct agg gct cga gca ggt ggt tta acg gtg gct gat agg cta aag 275
Lys Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys
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Lys Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu
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Gly Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly
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Gly	Val	Arg	Gln	Arg	Ile	Trp	Gly	Lys	Trp	Val	Ala	Glu	Ile	Arg	Glu	
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Pro	Lys	Ile	Gly	Thr	Arg	Leu	Trp	Leu	Gly	Thr	Phe	Pro	Thr	Ala	Glu	
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aaa	gct	gct	tcc	gct	tat	gat	gaa	gcg	gct	acc	gct	atg	tac	ggg	tca	563
Lys	Ala	Ala	Ser	Ala	Tyr	Asp	Glu	Ala	Ala	Thr	Ala	Met	Tyr	Gly	Ser	
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Thr	Ser	Ser	Gln	Ser	Glu	Val	Cys	Thr	Val	Glu	Asn	Lys	Ala	Val	Val	
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Cys	Gly	Asp	Val	Cys	Val	Lys	His	Glu	Asp	Thr	Asp	Cys	Glu	Ser	Asn	
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cca	ttt	agt	cag	att	tta	gat	ggt	aga	gaa	gag	tct	tgt	gga	acc	agg	755
Pro	Phe	Ser	Gln	Ile	Leu	Asp	Val	Arg	Glu	Glu	Ser	Cys	Gly	Thr	Arg	
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ccg	gac	agt	tgc	acg	ggt	gga	cat	caa	gat	atg	aat	tct	tcg	ctg	aat	803
Pro	Asp	Ser	Cys	Thr	Val	Gly	His	Gln	Asp	Met	Asn	Ser	Ser	Leu	Asn	
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Tyr	Asp	Leu	Leu	Leu	Glu	Phe	Glu	Gln	Gln	Tyr	Trp	Gly	Gln	Val	Leu	
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Gln	Glu	Lys	Glu	Lys	Pro	Lys	Gln	Glu	Glu	Glu	Glu	Ile	Gln	Gln	Gln	
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Gln	Gln	Glu	Gln	Gln	Gln	Gln	Gln	Leu	Gln	Pro	Asp	Leu	Leu	Thr	Val	
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275				280				285								
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 35 40 45  
 Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys  
 50 55 60  
 Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly  
 65 70 75 80  
 Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro  
 85 90 95  
 Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys  
 100 105 110  
 Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu  
 115 120 125  
 Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr  
 130 135 140  
 Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys  
 145 150 155 160  
 Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro  
 165 170 175  
 Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro  
 180 185 190  
 Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr  
 195 200 205  
 Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln  
 210 215 220  
 Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln Gln  
 225 230 235 240  
 Gln Glu Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala  
 245 250 255  
 Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser  
 260 265 270  
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 275 280 285  
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<400> 11

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<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 13

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<210> 14

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<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 14

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<211> 34

<212> DNA

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<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

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acgattaagg agaaatacaa ttcgaatgag aaggatgtgc cgtttgttat aataaacagc 540
cacacgacgt aaacgtaaaa tgaccacatg atgggccaat agacatggac cgactactaa 600
taatagtaag ttacatttta ggatggaata aatatcatac cgacatcagt tttgaaagaa 660
aagggaaaaa aagaaaaaat aaataaaaaga tatactaccg acatgagttc caaaaagcaa 720
aaaaaaagat caagccgaca cagacacgcg tagagagcaa aatgactttg acgtcacacc 780
acgaaaacag acgttctata cgtgtccctt tatctctctc agtctctcta taaacttagt 840
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<210> 22

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<212> DNA

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<210> 23

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<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

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